We claim:

1. A substantially purified nucleic acid molecule, said nucleic acid molecule capable of specifically hybridizing to a second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 82359 or complement or fragment of either.

2. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a microsatellite sequence.

3. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a region having a single nucleotide polymorphism.

4. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 82359 or complement thereof or fragment of either.

5. The substantially purified nucleic acid molecule according to claim 4, wherein said nucleic acid molecule further comprises a bacterial ORI site.

6. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule has a promoter or partial promoter region.

7. The substantially purified nucleic acid molecule according to claim 6, wherein said promoter region comprises a CAAT *cis* element and a TATA *cis* element and an additional *cis* element.

8. A substantially purified nucleic acid molecule comprising a nucleic acid molecule or fragment thereof having a pair of defined ends, wherein said pair of defined ends are selected from the defined ends in Table A.

9. The substantially purified nucleic acid molecule according to claim 8, wherein said molecule comprises a nucleic acid molecule having one or two of said defined ends.

10. The substantially purified nucleic acid molecule according to claim 9, wherein said molecule comprises a nucleic acid molecule having two of said defined ends.

11. A transformed plant having a nucleic acid molecule which comprises:

(A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; which is linked to

(B) a structural nucleic acid molecule, wherein said structural nucleic acid molecule is selected from the group consisting of SEQ ID NO:1 through SEQ ID NO: 82359 or complements thereof or fragment of either; which is linked to

(C) a 3' non-translated sequence that functions in a plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of said mRNA molecule.

12. The transformed plant according to claim 11, wherein said structural nucleic acid molecule is in the antisense orientation.

13. The transformed plant according to claim 11, wherein said plant is a dicot.

14. The transformed plant according to claim 11, wherein said plant is a monocot.

15. The transformed plant according to claim 11, wherein said plant is a maize plant.

16. A method for screening for a trait comprising interrogating genomic DNA for the presence or absence of a marker molecule that is genetically linked to a nucleic acid sequence complementary to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 82359 or complements thereof or fragment of either; and detecting said presence or absence of said marker.

17. The method for screening for enhanced yield according to claim 16, wherein said marker molecule is a microsatellite marker.

18. The method for screening for enhanced yield according to claim 16, wherein said marker molecule is a single nucleotide polymorphic marker.

19. The method for screening for enhanced yield according to claim 16, wherein said detecting of said presence or absence of said marker is detected by a detection method selected from the group consisting of AFLP, RFLP, RAPD, SNP and microsatellite analysis.

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